

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Ni, Jian  
Gentz, Reiner  
Yu, Guo-Liang  
Su, Jeffrey  
Rosen, Craig A.
- (ii) TITLE OF INVENTION: Death Domain Containing Receptor 5
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Human Genome Sciences, Inc.
  - (B) STREET: 9410 Key West Avenue
  - (C) CITY: Rockville
  - (D) STATE: MD
  - (E) COUNTRY: US
  - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US herewith
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/054,021
  - (B) FILING DATE: 29-JUL-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/040,846
  - (B) FILING DATE: 17-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Hoover, Kenley
  - (B) REGISTRATION NUMBER: 40,302
  - (C) REFERENCE/DOCKET NUMBER: PF366
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 3013098504
  - (B) TELEFAX: 3013098439

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1600 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 130..283

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 130..1362

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 284..1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACGCGTCCG CGGGCGCGGC CGGAGAACCC CGCAATCTTT GCGCCCAAA AATACACCGA	60
CGATGCCCGCA TCTACTTTAA GGGCTGAAAC CCACGGGCCT GAGAGACTAT AAGAGCGTTC	120
CCTACCGCC ATG GAA CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG	168
Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly	
-51 -50 -45 -40	
GCC CGG AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC AGG	216
Ala Arg Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg	
-35 -30 -25	
CCT GGG CCC CGG GTC CCC AAG ACC CTT GTG CTC GTT GTC GCC GCG GTC	264
Pro Gly Pro Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val	
-20 -15 -10	
CTG CTG TTG GTC TCA GCT GAG TCT GCT CTG ATC ACC CAA CAA GAC CTA	312
Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu	
-5 1 5 10	
GCT CCC CAG CAG AGA GCG GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA	360
Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser	
15 20 25	
GAG GGA TTG TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT	408
Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp	
30 35 40	
TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC TGG AAT GAC	456
Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp	
45 50 55	

CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT GAT TCA GGT GAA GTG GAG Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu 60 65 70	504
CTA AGT CCC TGC ACC ACG ACC AGA AAC ACA GTG TGT CAG TGC GAA GAA Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu 75 80 85 90	552
GGC ACC TTC CGG GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC Gly Thr Phe Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg 95 100 105	600
ACA GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA CCC TGG Thr Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp 110 115 120	648
AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC ATC ATC ATA GGA GTC Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val 125 130 135	696
ACA GTT GCA GCC GTA GTC TTG ATT GTG GCT GTG TTT GGT TGC AAG TCT Thr Val Ala Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser 140 145 150	744
TTA CTG TGG AAG AAA GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT Leu Leu Trp Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly 155 160 165 170	792
GGT GGT GGG GAC CCT GAG CGT <del>GTG-GAC</del> <u>AGA</u> AGC TCA CAA CGA CCT GGG Gly Gly Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly 175 180 185	840
GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC TTG CAG CCC ACC Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr 190 195 200	888
CAG GTC CCT GAG CAG GAA ATG GAA GTC CAG GAG CCA GCA GAG CCA ACA Gln Val Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr 205 210 215	936
GGT GTC AAC ATG TTG TCC CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG Gly Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro 220 225 230	984
GCA GAA GCT GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn 235 240 245 250	1032
GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT GAC TTT GCA Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala 255 260 265	1080
GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG CTC ATG AGG AAG TTG GGC Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly 270 275 280	1128

CTC ATG GAC AAT GAG ATA AAG GTG GCT AAA GCT GAG GCA GCG GGC CAC Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His 285 290 295	1176
AGG GAC ACC TTG TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly 300 305 310	1224
CGA GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG CTG GGA Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly 315 320 325 330	1272
GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC TTG TTG AGC TCT GGA Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly 335 340 345	1320
AAG TTC ATG TAT CTA GAA GGT AAT GCA GAC TCT GCC ATG TCC Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser 350 355 360	1362
TAAGTGTGAT TCTCTTCAGG AAGTGAGACC TTCCCTGGTT TACCTTTTTC CTGAAAAAAG	1422
CCCAACTGGA CTCCAGTCAG TAGGAAAGTG CCACAATTGT CACATGACCG GTACTGGAAG	1482
AAACTCTCCC ATCCAACATC ACCCAGTGGG TGGACATCC TGTAACCTTTT CACTGCACTT	1542
GGCATTATTT TTATAAGCTG AATGTGATAA TAAGGACACT ATGGAAAAAA AAAAAAAA	1600

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
-51 -50 -45 -40
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
-35 -30 -25 -20
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
-15 -10 -5
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
1 5 10
Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
15 20 25

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Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser  
 30 35 40 45  
 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe  
 50 55 60  
 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro  
 65 70 75  
 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe  
 80 85 90  
 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys  
 95 100 105  
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile  
 110 115 120 125  
 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala  
 130 135 140  
 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp  
 145 150 155  
 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly  
 160 165 170  
 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp  
 175 180 185  
 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro  
 190 195 200 205  
 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn  
 210 215 220  
 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala  
 225 230 235  
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp  
 240 245 250  
 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val  
 255 260 265  
 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp  
 270 275 280 285  
 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr  
 290 295 300  
 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala  
 305 310 315

Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu  
 320 325 330

Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met  
 335 340 345

Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser  
 350 355 360

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
 1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
 20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
 35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
 65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu

165	170	175
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr 180 185 190		
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser 195 200 205		
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu 210 215 220		
Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys 225 230 235 240		
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu 245 250 255		
Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser 260 265 270		
Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val 275 280 285		
Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys 290 295 300		
Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly 305 310 315 320		
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn 325 330 335		
Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp 340 345 350		
Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro 355 360 365		
Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu 370 375 380		
Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln 385 390 395 400		
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala 405 410 415		
Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly 420 425 430		
Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro 435 440 445		
Pro Ala Pro Ser Leu Leu Arg 450 455		

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1             5             10             15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
      20             25             30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
      35             40             45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
      50             55             60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
      65             70             75             80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
      85             90             95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
      100            105            110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
      115            120            125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
      130            135            140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
      145            150            155            160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
      165            170            175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
      180            185            190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
      195            200            205

```



Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu  
 210 215 220

Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met  
 225 230 235 240

Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu  
 245 250 255

Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu  
 260 265 270

Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys  
 275 280 285

Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys  
 290 295 300

Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser  
 305 310 315 320

Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val  
 325 330 335

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Leu Leu  
 1 5 10 15

Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg  
 20 25 30

Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys  
 35 40 45

Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro  
 50 55 60

Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala  
 65 70 75 80

Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp

[illegible]

Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met  
385 390 395 400

Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly  
405 410 415

Pro

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATTCGGCAC AGCTCTTCAG GAAGTCAGAC CTTCCTGGT TTACCTTTTT TCTGGA	50
AAAAA	
GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA	120
AGAAACTCTC CCATCCAACA TCACCCAGTG GNATGGGAAC ACTGATGAAC TTTTCACTGC	180
ACTTGGCATT ATTTTGTGNA AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG	240
ATCATTCGGG TTGTGCGTAC TTTGAGATT GNGTTGGGG ATGTNCATTG TGTGTGACAG	300
CACITTTTTN ATCCCTAATG TNAATGCNT NATTTGATTG TGANTGGGG GTNAACATTG	360
GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCGACT TANAATNGNN GAANANGATG	420
NATNANGAAC CTTTTTTTGG GTGGGGGGGT NNCGGGGCAG TTNAANGNNG NCTCCCCAGG	480
TTTGGNGTNG CAATNGNGGA ANNTTGG	507

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTGT AGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC ATTTACATTA 60  
 GGATAAAAAA GTGCTGTGAA AACAAATGACA TCCCAAACCA AATCTCAAAG TACGCACAAA 120  
 CGGAATGATC CAGACATTTC CATAGGTCCT TATTATCACA TTCAGCTTAT AAAAATATGC 180  
 CAAGTGCAGT GAAAAGTTAC AGGATGTTCC ATCCACTGGG TGGATT 226

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCCCATGGA GTCTGCTCTG ATCAC 25

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCAAGCTTT TAGCCTGATT CTTTGTTGAC 30

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGATCCG CCATCATGGA ACAACGGGGA CAGAAC

36

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGGTACCT TAGGACATGG CAGAGTC

27

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGGTACCT TAGCCTGATT CTTTGTGGAC

30